Amendments to the specification

Please amend the specification under the provisions of 37 C.F.R. §1.121(b)(1) as follows.

Following page 215, please add the paper copy of the "Sequence Listing", attached hereto as **Exhibit A.**

Please replace the paragraph beginning on page 16, line 31, with the following amended paragraph:

Figure 29D
Structure-based sequence alignment. Shown are the sequences of "HIV-1 B" (core gp120 from clade B, strain HXBc2 used in these studies) (SEQ ID NO:1), "C"(HIV-1 clade C, strain UG268A2) (SEQ ID NO:2), "0"(HIV-1 clade 0, strain ANT70) (SEQ ID NO:3), "HIV-2"(strain R0D) (SEQ ID NO:4), and "SIV" (African green monkey isolate, clone GRI-1) (SEQ ID NO:5). The secondary structure assignments are shown as arrows and cylinders, with (x) denoting residues which are disordered in the present structure. The "gars" sequence at the N-terminus and the "gag" sequence in the V1/V2 and V3 loops are consequences of the gp120 truncation. Solvent accessibility is indicated for each residue by an open circle if the fractional solvent accessibility is greater than 0.4, a half-closed circle if 0.1 to 0.4, and a closed circle if less than 0.1. Sequence variability observed among primate immunodeficiency viruses is indicated below the solvent accessibility by the number of horizontal hash marks: 1 mark, residues conserved among all primate

immunodeficiency viruses; 2 marks, conserved among all HIV-1 isolates; 3 marks, exhibits moderate variation among HIV-1 isolates; and 4 marks, exhibits significant variability among HIV-1 isolates. In accessing conservation, all single atom changes were permitted as well as larger substitutions if the character of the sidechain was conserved (e.g. K to R or F to L). N-linked glycosylation is indicated by "m" for the high mannose additions and "c" for the complex additions observed in mammalian cells (6). Residues of gp120 in direct contact with CD4 are indicated by"*". Direct contact is a more restrictive criterion of interaction than the often used loss of solvent accessible surface; residues of gp120 which show loss of solvent accessible surface but are not in direct contact are 123, 124, 126, 257, 278, 282, 364, 471, 475, 476 and 477. Parts (a) and (b) were drawn with MOLSCRIPT (P. J. Kraulis).

Please replace the paragraph beginning on page 29, line 11, with the following amended paragraph:

Figure 49
Schematic showing the structural domains of gp120 (SEQ ID NO:6).

Please replace the paragraph beginning on page 29, line 25, with the following amended paragraph:

Figure 53
Shows the x-ray crystallography obtained atomic coordinate data of the gp120 ternary complex of HIV-1

GP120 complexed with CD4 and Fab 17b (SEQ ID NOS:7-13) having space group P2221 and unit cell dimensions a=71.643, b=88.130,c = 196.7. The raw data and the coordinates were described in U.S. Serial No. 09/100,764, filed June 18, 1998 and U.S. Serial No. 08/967,708, filed November 10, 1997, on which this subject application claims priority. These documents are subjected for public inspection. The contents of these applications are incorporated into this application by reference. The coordinates have been deposited in the in the Brookhaven Protein Data Bank with the accession code Igcl. In addition, the coordinates may be obtained in the worldwide web: www.pbd.bnl.gov after inputting "Igcl" for the above coordinates.